COL 786 - Assignment 5: Develop General Linear Model Analysis Tool for fMRI Data

Due Date: 7:00pm, Sunday, 27th April, 2025
Max Marks : 100

Notes: The objective of this assignment is to develop a command-line-based tool for General Linear Model (GLM) Analysis of fMRI data. The tool has two parts. The first part aims to develop a GLM tool for single-subject analysis. The second part aims to develop a GLM tool for group analysis.

1 Tool for Single Subject GLM Analysis [60 Marks]

Create a Python command line tool with the name `glm.py` with the following specifications:
`python glm.py <functional file> <ev file> <contrast file> <output prefix>`
Your Python program takes 4 arguments: The first argument is the `<functional file>` which is the name of the filtered and preprocessed 4-dimensional input fMRI data. The second argument is the `<ev file>` which represents the different experimental conditions. The experimental variables of EVs are in a four-column format with the following interpretation: the first column represents the start of an experimental condition or a block (in seconds), the second column represents the duration of the experimental condition (in seconds), the third column represents the value of the experimental condition in the given time interval and the fourth column has an integer representing the experimental condition number. If there are three different types of experimental conditions, then the fourth column may take values of 1, 2, and 3 representing the three experimental conditions. The `<contrast file>` contains a list of numbers in each row with a first number corresponding to the first EV, the second number corresponding to the second EV, and so on. If there are a total of three experimental conditions, then each row of the `<contrast file>` will contain three numbers representing the weight of each experimental condition in this contrast. Each row in the `<contrast file>` corresponds to a different contrast value.
Your program should create output files with the name beginning with the `<output prefix>`. The files that are to be created are:

1. Parameter estimate files (betas): `<output prefix>.pe<1>.nii.gz` to `<output prefix>.pe<n>.nii.gz` representing different experimental conditions. The number of pe files must be equal to the number of EVs in the `<ev file>`.

2. Contrast of parameter estimation files: `<output prefix>.cope<1>.nii.gz` to `<output prefix>.cope<m>.nii.gz` representing the contrast of parameter estimates ($c^t\beta$). The number of cope files should be equal to the number of rows in the `<contrast file>`.

3. t-statistics files: `<output prefix>.tstat<1>.nii.gz` to `<output prefix>.tstat<m>.nii.gz` representing the t-statistics of the contrast of parameter estimate. The number of tstat files should be equal to the number of rows in the `<contrast file>`.

4. z-statistics files: `<output prefix>.zstat<1>.nii.gz` to `<output prefix>.zstat<m>.nii.gz` representing the z-statistics of the contrast of parameter estimate. The t-statistics should be converted to a standard z-statistics value and stored in the zstat files for each of the contrasts. The number of zstat files should be equal to the number of rows in the `<contrast file>`.

Use your tool to generate every contrast in your assignment 2 for one of the subjects. Create a report comparing the parameter estimate files and the zstat files generated by your program with the corresponding files generated by the FSL tool. For comparison, carry out a scatter plot of the PE (and zstat) values for every voxel in the brain with x-axis as the PE (or zstat) value as computed by FSL and y-axis as the values calculated by your program.

Also, include brain maps of the zstat files (FSL computed and computed by your program) for a side-by-side comparison.

Submission Instructions: You need to submit your program `glm.py` and the input `<ev file>` and `<contrast file>` on moodle and your report on gradescope. In case your results don't match the FSL results, try to explain why they are different. Your evaluation will be based on the correctness of your program and the quality of your report.

2   Tool for Group Analysis [40 Marks]

Create a Python command line tool with the name `group_analysis.py` to carry out group analysis of fMRI data with the following specifications:

`python group_analysis.py <file list.txt> <output prefix>`.

Your program takes two arguments. The `<file list.txt>` is a file containing the list of registered file names on which the group analysis is to be done. These files may be parameter estimate (pe) files, contrast of parameter estimate (cope) files, or zstat files generated during the first level analysis. The program should assume that all the files are registered to a standard atlas and carry out an independent t-test for every test for every voxel. The null hypothesis assumes that the voxel values are normally distributed with a zero mean and unknown variance and different files represent different independently and identically distributed samples of the variables. Your program should output the following files:

1. t-statistics file: `<output prefix>.tstat.nii.gz>` contains the t-statistic value for every voxel in the brain after the group-level hypothesis testing.

2. z-statistics file: `<output prefix>.zstat.nii.gz>` contains the z-statistics value converted from the t-statistic value.

Use your tool to generate every contrast in your assignment 2 for all the subjects that you analyzed in your assignment 3. Register the cope files to the standard atlas using the affine transformation (the mat files) of your assignment 3, and the FSL registration tool flirt (use the option -applyxfm to register using an existing affine transformation file). Now carry out the group level analysis using the `group_analysis.py` developed by you on the registered files. For group-level analysis, you will test against the null hypothesis of beta (cope) = 0.

Create a report comparing the group-level zstat files generated by your program with the corresponding files generated by the FSL tool for each of the contrasts that you studied. For comparison, carry out a scatter plot of zstat values for every voxel in the brain with the x-axis as the group zstat value as computed by FSL and the y-axis as the values calculated by your program. Also, include brain maps of the zstat files for a side-by-side comparison.

Submission Instructions: You need to submit your program `group_analysis.py` on moodle and your report on gradescope. In your report, include a link to the drive that has your intermediate PE, tstat, and zstat files and final group-level tstat and zstat files for your contrasts. In case your results don't match the FSL results, try to explain why they are different. Your evaluation will be based on the correctness of your program and the quality of your report.

COL 786 - Advanced Functional Brain Imaging - Assignment 5 (Cognitive Science Stream)

Functional Connectivity Analysis using the CONN toolbox

Notes: The objective of this assignment is to understand functional connectivity analysis and perform the functional connectivity analysis on the Brainiommics data using the CONN toolbox.

1 Background

Read the following papers to build your background.

1. Bastos, André M., and Jan-Mathijs Schoffelen. "A tutorial review of functional connectivity analysis methods and their interpretational pitfalls." Frontiers in systems neuroscience 9 (2016): 175.

2. Resting state functional connectivity playlist

3. Hutchison, R. Matthew, et al. "Dynamic functional connectivity: promise, issues, and interpretations." Neuroimage 80 (2013): 360-378.

4. Menon, Vinod. "20 years of the default mode network: A review and synthesis." Neuron 111.16 (2023): 2469-2487.

5. The CONN Tool Box to compute functional connectivity (please see documentations and tutorials)

6. Functional Connectivity and the CONN Toolbox

2 Use the CONN toolbox for pre-processing of Brainomics/Localizer database of (A3). Use the tool to calculate group functional connectivity maps and group contrasts (100 marks)

1. Literature Review **(20 Marks)**: Begin your report with a brief review of the literature on functional connectivity and default mode networks. Describe different methods to carry out functional connectivity analysis. What are default mode networks (DMNs) and how our understanding of DMNs has evolved over the past 20 years. How functional connectivity analysis may help discover the DMNs.

2. Preprocessing data using the CONN toollbox **(20 Marks)**. Pre-process the **Brainomics/Localizer** data using the CONN toollbox. In detail, describe various pre-processing steps applied to the fMRI data. Also, include various pre-processing parameters used in this step. Ensure that the fMRI data of each subject is registered in a common template brain, i.e., MNI152 and create a report of inspection of registration.

3. Individual-subject Functional Connectivity Analysis **(30 Marks):**

   - Perform the functional connectivity analysis using the CONN toolbox.
   - Generate functional connectivity maps for the following four regions:
     (a) Left Brodmann area 44 (pars opercularis of the inferior frontal gyrus).
     (b) Right Brodmann area 44 (pars opercularis of the inferior frontal gyrus).
     (c) Left Brodmann area 45 (pars triangularis).
     (d) Right Brodmann area 45 (pars triangularis).

Note that, pars opercularis along with pars triangularis of the left hemisphere constitute what is called Broca's area in the brain. Your objective is to create individual functional connectivity maps for the above four regions for good subjects. Click here for a list of 90 good subjects for which the analysis needs to be run (if you are unable to run on these 90 subjects, then you may run on 30 good subjects shared earlier).

4. **Group level functional connectivity analysis using the CONN toolbox (30 Marks):** Use the group analysis of the CONN toolbox to generate the following functional connectivity contrasts.

   (a) FC of left Brodmann area 44 (pars opercularis of the inferior frontal gyrus).

   (b) FC of right Brodmann area 44 (pars opercularis of the inferior frontal gyrus).

   (c) FC of left Brodmann area 45 (pars triangularis).

   (d) FC of right Brodmann area 45 (pars triangularis).

   (e) FC of left Brodmann area 44 minus the FC of right Brodmann area 44

   (f) FC of left Brodmann area 45 minus the FC of right Brodmann area 45

   Use your knowledge of neuroscience to explain the that you obtain. You are free to consult the online and AI tools for helping to come up with an explanation of your results.

3   Submission Instructions

You need to submit your report on gradescope. For part (1) your report needs to detail the literature review. For part (2), clearly indicate the detailed steps performed by you on the CONN tool box during your analysis (include the screenshot of the CONN toolbox along with parameter settings). Clearly specify the pre-processing parameters used by you for the analysis. Also include a drive link to all your raw as well as pre-processed data. Make sure that the date of any of the files in the sub-directory is not changed after you do the submission.

For part (3) include the functional connectivity brain map for one of the subjects along with its cluster table. For each of the four regions of FC, include one figure and one table that you obtain for your subject. Also include a link to your raw data, pro-processed data and your final results.

For part (4) include suitably formatted FDR corrected brain maps and cluster table (FDR corrected) for each of the six contrasts generated by you. This must be followed by discussions on explaining your results and putting these in perspective with the prior knowledge in Neuroscience.

In your report, include suitable links to the drive that has your intermediate results such as the raw files downloaded, pre-processed files, intermediate and final results. Your report quality depends on the quality of figures and tables depicting your findings and your ability to interpret your findings in the context of known results on the topic.